

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/945,327

DATE: 11/07/2001

TIME: 14:35:12

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11072001\I945327.raw

3 <110> APPLICANT: Meyers, Rachel  
 5 <120> TITLE OF INVENTION: 50566, A NOVEL HUMAN GLYOXALASE II RELATED FACTOR AND  
 6 USES THEREOF  
 8 <130> FILE REFERENCE: MNI-185  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/945,327  
 C--> 11 <141> CURRENT FILING DATE: 2001-08-31  
 13 <150> PRIOR APPLICATION NUMBER: 60/229,425  
 14 <151> PRIOR FILING DATE: 2000-08-31  
 16 <160> NUMBER OF SEQ ID NOS: 3  
 18 <170> SOFTWARE: PatentIn Ver. 2.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1154  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (22)..(870)  
 29 <400> SEQUENCE: 1  
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 31 Met Lys Val Lys Val Ile Pro Val Leu Glu  
 32 1 5 10  
 34 gac aac tac atg tac ctg gtc atc gag gag ctc acg cgc gag gcg gtg 99  
 35 Asp Asn Tyr Met Tyr Leu Val Ile Glu Glu Leu Thr Arg Glu Ala Val  
 36 15 20 25  
 38 gcc gtg gac gtg gct gtg ccc aag agg ctg ctg gag atc gtg ggc cgg 147  
 39 Ala Val Asp Val Ala Val Pro Lys Arg Leu Leu Glu Ile Val Gly Arg  
 40 30 35 40  
 42 gag ggg gtg tct ctg acc gct gtg ctg acc acc cac cat cac tgg gac 195  
 43 Glu Gly Val Ser Leu Thr Ala Val Leu Thr Thr His His His Trp Asp  
 44 45 50 55  
 46 cac gcg cgg gga aac ccg gag ctg gcg cgg ctt cgt ccc ggg ctg gcg 243  
 47 His Ala Arg Gly Asn Pro Glu Leu Ala Arg Leu Arg Pro Gly Leu Ala  
 48 60 65 70  
 50 gtg ctg ggc gcg gac gag cgc atc ttc tcg ctg acg cgc agg ctg gcg 291  
 51 Val Leu Gly Ala Asp Glu Arg Ile Phe Ser Leu Thr Arg Arg Leu Ala  
 52 75 80 85 90  
 54 cac ggc gag gag ctg cgg ttc ggg gcc atc cac gtg cgt tgc ctc ctg 339  
 55 His Gly Glu Glu Leu Arg Phe Gly Ala Ile His Val Arg Cys Leu Leu  
 56 95 100 105  
 58 acg ccc ggc cac acc gcc ggc cac atg agc tac ttc ctg tgg gag gac 387  
 59 Thr Pro Gly His Thr Ala Gly His Met Ser Tyr Phe Leu Trp Glu Asp  
 60 110 115 120  
 62 gat tgc ccg gac cca ccc gcc ctg ttc tcg ggc gac gcg ctg tcg gtg 435  
 63 Asp Cys Pro Asp Pro Pro Ala Leu Phe Ser Gly Asp Ala Leu Ser Val  
 64 125 130 135  
 66 gcc ggc tgc ggc tcg tgc ctg gag ggc agc gcc cag cag atg tac cag 483  
 67 Ala Gly Cys Gly Ser Cys Leu Glu Gly Ser Ala Gln Gln Met Tyr Gln

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70 agc ctg gcc gag ctg ggt acc ctg ccc ccc gag acg aag gtg ttc tgc 531
71 Ser Leu Ala Glu Leu Gly Thr Leu Pro Pro Glu Thr Lys Val Phe Cys
72 155      160      165      170
74 ggc cac gag cac acg ctt agc aac ctg gag ttt gcc cag aaa gtg gag 579
75 Gly His Glu His Thr Leu Ser Asn Leu Glu Phe Ala Gln Lys Val Glu
76      175      180      185
78 ccc tgc aac gac cac gtg aga gcc aag ctg tcc tgg gct aag aag agg 627
79 Pro Cys Asn Asp His Val Arg Ala Lys Leu Ser Trp Ala Lys Lys Arg
80      190      195      200
82 gat gag gat gac gtg ccc act gtg ccg tcg act ctg ggc gag gag cgc 675
83 Asp Glu Asp Asp Val Pro Thr Val Pro Ser Thr Leu Gly Glu Glu Arg
84      205      210      215
86 ctc tac aac ccc ttc ctg cgg gtg gca gag gag ccg gtg cgc aag ttc 723
87 Leu Tyr Asn Pro Phe Leu Arg Val Ala Glu Glu Pro Val Arg Lys Phe
88      220      225      230
90 acg ggc aag gcg gtc ccc gcc gac gtc ctg gag gcg cta tgc aag gag 771
91 Thr Gly Lys Ala Val Pro Ala Asp Val Leu Glu Ala Leu Cys Lys Glu
92 235      240      245      250
94 cgg gcg cgc ttc gaa cag gcg ggc gag ccg cgg cag cca cag gcg cgg 819
95 Arg Ala Arg Phe Glu Gln Ala Gly Glu Pro Arg Gln Pro Gln Ala Arg
96      255      260      265
98 gcc ctc ctt gcg ctg cag tgg ggg ctc ctg agt gca gcc cca cac gac 867
99 Ala Leu Leu Ala Leu Gln Trp Gly Leu Leu Ser Ala Ala Pro His Asp
100      270      275      280
102 tga gccacccaga ccctcacagg gctggggcct gcgtccctcc tcgtgacctc 920
105 ggccagctgg accacatga gggccacctc tggaaccttc ttcgaggccc tggccagcca 980
107 tctgcccagc ctcgagggt gggcaacctg gtgcttccc ggtggacaca caggaccact 1040
109 cagtggggcc tgtgtgggcg ccgagacctg ggtgtctggg aagtggggca cacggggcct 1100
111 ccgaactatg aataaagctt tgaaagccgt tgtcaaaaaa aaaaaaaaaa aaaa 1154
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115 <211> LENGTH: 282
116 <212> TYPE: PRT
117 <213> ORGANISM: Homo sapiens
119 <400> SEQUENCE: 2
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123 Val Ile Glu Glu Leu Thr Arg Glu Ala Val Ala Val Asp Val Ala Val
124 20 25 30
126 Pro Lys Arg Leu Leu Glu Ile Val Gly Arg Glu Gly Val Ser Leu Thr
127 35 40 45
129 Ala Val Leu Thr Thr His His His Trp Asp His Ala Arg Gly Asn Pro
130 50 55 60
132 Glu Leu Ala Arg Leu Arg Pro Gly Leu Ala Val Leu Gly Ala Asp Glu
133 65 70 75 80
135 Arg Ile Phe Ser Leu Thr Arg Arg Leu Ala His Gly Glu Glu Leu Arg
136 85 90 95
138 Phe Gly Ala Ile His Val Arg Cys Leu Leu Thr Pro Gly His Thr Ala
139 100 105 110

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141 Gly His Met Ser Tyr Phe Leu Trp Glu Asp Asp Cys Pro Asp Pro Pro
142      115                      120                      125
144 Ala Leu Phe Ser Gly Asp Ala Leu Ser Val Ala Gly Cys Gly Ser Cys
145      130                      135                      140
147 Leu Glu Gly Ser Ala Gln Gln Met Tyr Gln Ser Leu Ala Glu Leu Gly
148 145                      150                      155                      160
150 Thr Leu Pro Pro Glu Thr Lys Val Phe Cys Gly His Glu His Thr Leu
151      165                      170                      175
153 Ser Asn Leu Glu Phe Ala Gln Lys Val Glu Pro Cys Asn Asp His Val
154      180                      185                      190
156 Arg Ala Lys Leu Ser Trp Ala Lys Lys Arg Asp Glu Asp Asp Val Pro
157      195                      200                      205
159 Thr Val Pro Ser Thr Leu Gly Glu Glu Arg Leu Tyr Asn Pro Phe Leu
160      210                      215                      220
162 Arg Val Ala Glu Glu Pro Val Arg Lys Phe Thr Gly Lys Ala Val Pro
163 225                      230                      235                      240
165 Ala Asp Val Leu Glu Ala Leu Cys Lys Glu Arg Ala Arg Phe Glu Gln
166      245                      250                      255
168 Ala Gly Glu Pro Arg Gln Pro Gln Ala Arg Ala Leu Leu Ala Leu Gln
169      260                      265                      270
171 Trp Gly Leu Leu Ser Ala Ala Pro His Asp
172      275                      280
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 846
177 <212> TYPE: DNA
178 <213> ORGANISM: Homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)..(846)
184 <400> SEQUENCE: 3
185 atg aag gtc aag gtc atc ccc gtg ctc gag gac aac tac atg tac ctg 48
186 Met Lys Val Lys Val Ile Pro Val Leu Glu Asp Asn Tyr Met Tyr Leu
187 1 5 10 15
189 gtc atc gag gag ctc acg cgc gag gcg gtg gcc gtg gac gtg gct gtg 96
190 Val Ile Glu Glu Leu Thr Arg Glu Ala Val Ala Val Asp Val Ala Val
191 20 25 30
193 ccc aag agg ctg ctg gag atc gtg ggc cgg gag ggg gtg tct ctg acc 144
194 Pro Lys Arg Leu Leu Glu Ile Val Gly Arg Glu Gly Val Ser Leu Thr
195 35 40 45
197 gct gtg ctg acc acc cac cat cac tgg gac cac gcg cgg gga aac ccg 192
198 Ala Val Leu Thr Thr His His His Trp Asp His Ala Arg Gly Asn Pro
199 50 55 60
201 gag ctg gcg cgg ctt cgt ccc ggg ctg gcg gtg ctg ggc gcg gac gag 240
202 Glu Leu Ala Arg Leu Arg Pro Gly Leu Ala Val Leu Gly Ala Asp Glu
203 65 70 75 80
205 cgc atc ttc tcg ctg acg cgc agg ctg gcg cac ggc gag gag ctg cgg 288
206 Arg Ile Phe Ser Leu Thr Arg Arg Leu Ala His Gly Glu Glu Leu Arg
207 85 90 95
209 ttc ggg gcc atc cac gtg cgt tgc ctc ctg acg ccc ggc cac acc gcc 336

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210	Phe	Gly	Ala	Ile	His	Val	Arg	Cys	Leu	Leu	Thr	Pro	Gly	His	Thr	Ala	
211				100					105				110				
213	ggc	cac	atg	agc	tac	ttc	ctg	tgg	gag	gac	gat	tgc	ccg	gac	cca	ccc	384
214	Gly	His	Met	Ser	Tyr	Phe	Leu	Trp	Glu	Asp	Asp	Cys	Pro	Asp	Pro	Pro	
215		115						120					125				
217	gcc	ctg	ttc	tgc	ggc	gac	gcg	ctg	tgc	gtg	gcc	ggc	tgc	ggc	tgc	tgc	432
218	Ala	Leu	Phe	Ser	Gly	Asp	Ala	Leu	Ser	Val	Ala	Gly	Cys	Gly	Ser	Cys	
219		130						135					140				
221	ctg	gag	ggc	agc	gcc	cag	cag	atg	tac	cag	agc	ctg	gcc	gag	ctg	ggt	480
222	Leu	Glu	Gly	Ser	Ala	Gln	Gln	Met	Tyr	Gln	Ser	Leu	Ala	Glu	Leu	Gly	
223	145					150					155					160	
225	acc	ctg	ccc	ccc	gag	acg	aag	gtg	ttc	tgc	ggc	cac	gag	cac	acg	ctt	528
226	Thr	Leu	Pro	Pro	Glu	Thr	Lys	Val	Phe	Cys	Gly	His	Glu	His	Thr	Leu	
227					165					170					175		
229	agc	aac	ctg	gag	ttt	gcc	cag	aaa	gtg	gag	ccc	tgc	aac	gac	cac	gtg	576
230	Ser	Asn	Leu	Glu	Phe	Ala	Gln	Lys	Val	Glu	Pro	Cys	Asn	Asp	His	Val	
231			180						185				190				
233	aga	gcc	aag	ctg	tcc	tgg	gct	aag	aag	agg	gat	gag	gat	gac	gtg	ccc	624
234	Arg	Ala	Lys	Leu	Ser	Trp	Ala	Lys	Lys	Arg	Asp	Glu	Asp	Asp	Val	Pro	
235		195						200				205					
237	act	gtg	ccg	tgc	act	ctg	ggc	gag	gag	cgc	ctc	tac	aac	ccc	ttc	ctg	672
238	Thr	Val	Pro	Ser	Thr	Leu	Gly	Glu	Glu	Arg	Leu	Tyr	Asn	Pro	Phe	Leu	
239		210					215					220					
241	cgg	gtg	gca	gag	gag	ccg	gtg	cgc	aag	ttc	acg	ggc	aag	gcg	gtc	ccc	720
242	Arg	Val	Ala	Glu	Glu	Pro	Val	Arg	Lys	Phe	Thr	Gly	Lys	Ala	Val	Pro	
243	225					230					235				240		
245	gcc	gac	gtc	ctg	gag	gcg	cta	tgc	aag	gag	cgg	gcg	cgc	ttc	gaa	cag	768
246	Ala	Asp	Val	Leu	Glu	Ala	Leu	Cys	Lys	Glu	Arg	Ala	Arg	Phe	Glu	Gln	
247			245						250				255				
249	gcg	ggc	gag	ccg	cgg	cag	cca	cag	gcg	cgg	gcc	ctc	ctt	gcg	ctg	cag	816
250	Ala	Gly	Glu	Pro	Arg	Gln	Pro	Gln	Ala	Arg	Ala	Leu	Leu	Ala	Leu	Gln	
251			260						265				270				
253	tgg	ggg	ctc	ctg	agt	gca	gcc	cca	cac	gac							846
254	Trp	Gly	Leu	Leu	Ser	Ala	Ala	Pro	His	Asp							
255			275						280								

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/945,327

DATE: 11/07/2001

TIME: 14:35:14

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11072001\I945327.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date